

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: INCYTE PHARMACEUTICALS, INC.  
(ii) TITLE OF THE INVENTION: NOVEL HUMAN MAGE-LIKE PROTEIN  
(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.  
(B) STREET: 3174 Porter Drive  
(C) CITY: Palo Alto  
(D) STATE: CA  
(E) COUNTRY: USA  
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) pct APPLICATION NUMBER: To Be Assigned  
(B) FILING DATE: Herewith  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: us 08/773,870  
(B) FILING DATE: 27-DEC-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Billings, Lucy J.  
(B) REGISTRATION NUMBER: 36,749  
(C) REFERENCE/DOCKET NUMBER: PF-0179 PCT

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650-855-0555  
(B) TELEFAX: 650-845-4166  
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 411 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(A) LIBRARY: Consensus

## (B) CLONE: Consensus

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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Met Ala Phe Pro Arg Pro Lys Lys Asn Leu Pro Gln Pro Lys Xaa Ala
 1           5           10           15
Ala Thr Glu Gly Pro Ser Ala Ala Ser Gly Val Pro Gln Thr Gly Pro
 20          25           30
Gly Arg Glu Val Ala Ala Thr Arg Pro Lys Thr Thr Lys Ser Gly Lys
 35          40           45
Ala Leu Ala Lys Thr Arg Trp Val Glu Pro Gln Asn Val Val Ala Ala
 50          55           60
Ala Ala Ala Lys Ala Lys Met Ala Thr Ser Ile Pro Glu Pro Glu Gly
 65          70           75           80
Ala Ala Ala Ala Thr Ala Gln His Ser Ala Glu Pro Trp Ala Arg Met
 85          90           95
Gly Gly Lys Arg Thr Lys Lys Ser Lys His Leu Asp Asp Glu Tyr Glu
100         105          110
Ser Ser Glu Glu Glu Arg Glu Thr Pro Ala Val Pro Pro Thr Trp Arg
115         120          125
Ala Ser Gln Pro Ser Leu Thr Val Arg Ala Gln Leu Ala Pro Arg Pro
130         135          140
Pro Met Ala Pro Arg Ser Gln Ile Pro Ser Arg His Val Leu Cys Leu
145         150          155           160
Pro Pro Arg Asn Val Thr Leu Leu Gln Glu Arg Ala Asn Lys Leu Val
165         170          175
Lys Tyr Leu Met Ile Lys Asp Tyr Lys Lys Ile Pro Ile Lys Arg Ala
180         185          190
Asp Met Leu Lys Asp Val Ile Arg Glu Tyr Asp Glu His Phe Pro Glu
195         200          205
Ile Ile Glu Arg Ala Thr Tyr Thr Leu Glu Lys Lys Phe Gly Ile His
210         215          220
Leu Lys Glu Ile Asp Lys Glu Glu His Leu Tyr Ile Leu Val Cys Thr
225         230          235           240
Arg Asp Ser Ser Ala Arg Leu Leu Gly Lys Thr Lys Asp Thr Pro Arg
245         250          255
Leu Ser Leu Leu Val Ile Leu Gly Val Ile Phe Met Asn Gly Asn
260         265          270
Arg Ala Ser Glu Ala Val Leu Trp Glu Ala Leu Arg Lys Met Gly Leu
275         280          285
Arg Pro Gly Val Arg His Pro Leu Leu Gly Asp Leu Arg Lys Leu Leu
290         295          300
Thr Tyr Glu Phe Val Lys Gln Lys Tyr Leu Asp Tyr Arg Arg Val Pro
305         310          315           320
Asn Ser Asn Pro Pro Glu Tyr Glu Phe Leu Trp Gly Leu Arg Ser Tyr
325         330          335
His Glu Thr Ser Lys Met Lys Val Leu Arg Phe Ile Ala Glu Val Gln
340         345          350
Lys Arg Asp Pro Arg Asp Trp Thr Ala Gln Phe Met Glu Ala Ala Asp
355         360          365
Glu Ala Leu Asp Ala Leu Asp Ala Ala Ala Glu Ala Glu Ala Arg
370         375          380
Ala Glu Ala Arg Thr Arg Met Gly Ile Gly Asp Glu Ala Val Ser Gly
385         390          395           400
Pro Gly Ala Gly Met Thr Leu Ser Leu Ser Cys

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405

410

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Consensus
- (B) CLONE: Consensus

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CNACGNGAAT	GGCCTTCCCG	CGCCCCAAGA	AGAACCTGCC	CCAGCCAAG	NAGGCTGCCA	60
CAGAGGGGCC	CAGTGCTGCC	TCTGGTGTGC	CCCAGACGGG	ACCTGGCAGG	GAGGTGGCAG	120
CCACCCGGCC	CAAGACCACC	AAGTCGGGGA	AGGCGCTGGC	CAAGACTCGG	TGGGTGGAGC	180
CTCAGAATGT	TGTGGCAGCA	GCTGCTGCCA	AGGCCAAGAT	GGCCACGAGC	ATCCCTGAGC	240
CGGAGGGTGC	AGCTGCTGCC	ACTGCTCAGC	ACAGTGCTGA	GCCCTGGGCC	AGGATGGGAG	300
GCAAGAGGAC	CAAGAAGTCC	AAGCACCTGG	ATGATGAGTA	TGAGAGCAGC	GAGGAGGAGA	360
GAGAGACTCC	CGCGGTCCCA	CCCACCTGGA	GAGCATCACA	GCCCTCATTTG	ACGGTGCAGG	420
CTCAGTTGGC	CCCTCGGCC	CCGATGGCCC	CGAGGTCCCA	GATACCCCTCA	AGGCACGTAC	480
TGTGCCTGCC	CCCCCGCAAC	GTGACCCCTTC	TGCAAGGAGAG	GGCAAATAAG	TTGGTGAAAT	540
ACCTGATGAT	TAAGGACTAC	AAGAAGATCC	CCATCAAGCG	CGCAGACATG	CTGAAGGATG	600
TCATCAGAGA	ATATGATGAA	CATTTCCCTG	AGATCATTGA	ACGAGCAACG	TACACCCTGG	660
AAAAGAAGTT	TGGGATCCAC	CTGAAGGAGA	TCGACAAGGA	AGAACACCTG	TATATTCTTG	720
TCTGCACACG	GGACTCCTCA	GCTCGCCCTCC	TTGGAAAAAC	CAAGGACACT	CCCAGGCTGA	780
GTCTCCTCTT	GGTGATTCTG	GGCGTCATCT	TCATGAATGG	CAACCGTGCC	AGCGAGGCTG	840
TCCTCTGGGA	GGCACTACGC	AAGATGGGAC	TGGCTCCTGG	GGTGAGACAT	CCCCTCCTTG	900
GAGATCTAAG	GAAACTTCTC	ACCTATGAGT	TTGTAAGCA	GAAATACCTG	GACTACAGAC	960
GAGTGCCCAA	CAGCAACCCC	CCGGAGATG	AGTTCTCTG	GGGCCTCCGT	TCCTACCATG	1020
AGACTAGCAA	GATGAAAGTG	CTGAGATTCA	TTGCAGAGGT	TCAGAAAAGA	GACCCTCGTG	1080
ACTGGACTGC	ACAGTTCATG	GAGGCTGCAG	ATGAGGCCTT	GGATGCTCTG	GATGCTGCTG	1140
CAGCTGAGGC	CGAAGCCCGG	GCTGAAGCAA	GAACCCGCAT	GGGAATTGGA	GATGAGGCTG	1200
TGTCTGGGCC	CGGAGCTGGG	ATGACATTGA	TTTGAGCTG	CTGACCT		1247

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 608993

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Pro	Arg	Gly	Gln	Lys	Ser	Lys	Leu	Arg	Ala	Arg	Glu	Lys	Arg	Arg
1															15
Lys	Ala	Arg	Glu	Glu	Thr	Gln	Gly	Leu	Lys	Val	Arg	His	Ala	Thr	Ala

20	25	30
Ala Glu Lys Glu Glu Cys Pro Ser Ser Ser Pro Val Leu Gly Asp Thr		
35	40	45
Pro Thr Ser Ser Pro Ala Ala Gly Ile Pro Gln Lys Pro Gln Gly Ala		
50	55	60
Pro Pro Thr Thr Thr Ala Ala Ala Val Ser Cys Thr Glu Ser Asp		
65	70	75
80		
Glu Gly Ala Lys Cys Gln Gly Glu Glu Asn Ala Ser Phe Ser Gln Ala		
85	90	95
Thr Thr Ser Thr Glu Ser Ser Val Lys Asp Pro Val Ala Trp Glu Ala		
100	105	110
Gly Met Leu Met His Phe Ile Leu Arg Lys Tyr Lys Met Arg Glu Pro		
115	120	125
Ile Met Lys Ala Asp Met Leu Lys Val Val Asp Glu Lys Tyr Lys Asp		
130	135	140
His Phe Thr Glu Ile Leu Asn Gly Ala Ser Arg Arg Leu Glu Leu Val		
145	150	155
160		
Phe Gly Leu Asp Leu Lys Glu Asp Asn Pro Ser Ser His Thr Tyr Thr		
165	170	175
Leu Val Ser Lys Leu Asn Leu Thr Asn Asp Gly Asn Leu Ser Asn Asp		
180	185	190
Trp Asp Phe Pro Arg Asn Gly Leu Leu Met Pro Leu Leu Gly Val Ile		
195	200	205
Phe Leu Lys Gly Asn Ser Ala Thr Glu Glu Glu Ile Trp Lys Phe Met		
210	215	220
Asn Val Leu Gly Ala Tyr Asp Gly Glu Glu His Leu Ile Tyr Gly Glu		
225	230	235
240		
Pro Arg Lys Phe Ile Thr Gln Asp Leu Val Gln Glu Lys Tyr Leu Lys		
245	250	255
Tyr Glu Gln Val Pro Asn Ser Asp Pro Pro Arg Tyr Gln Phe Leu Trp		
260	265	270
Gly Pro Arg Ala Tyr Ala Glu Thr Thr Lys Met Lys Val Leu Glu Phe		
275	280	285
Leu Ala Lys Met Asn Gly Ala Thr Pro Arg Asp Phe Pro Ser His Tyr		
290	295	300
Glu Glu Ala Leu Arg Asp Glu Glu Glu Arg Ala Gln Val Arg Ser Ser		
305	310	315
320		
Val Arg Ala Arg Arg Arg Thr Thr Ala Thr Thr Phe Arg Ala Arg Ser		
325	330	335
Arg Ala Pro Phe Ser Arg Ser Ser His Pro Met		
340	345	

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 533511

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Pro Arg Ala Pro Lys Arg Gln Arg Cys Met Pro Glu Glu Asp Leu  
 1 5 10 15  
 Gln Ser Gln Ser Glu Thr Gln Gly Leu Glu Gly Ala Gln Ala Pro Leu  
 20 25 30  
 Ala Val Glu Glu Asp Ala Ser Ser Ser Thr Ser Thr Ser Ser Ser Phe  
 35 40 45  
 Pro Ser Ser Phe Pro Ser Ser Ser Ser Ser Ser Ser Ser Cys Tyr  
 50 55 60  
 Pro Leu Ile Pro Ser Thr Pro Glu Glu Val Ser Ala Asp Asp Glu Thr  
 65 70 75 80  
 Pro Asn Pro Pro Gln Ser Ala Gln Ile Ala Cys Ser Ser Pro Ser Val  
 85 90 95  
 Val Ala Ser Leu Pro Leu Asp Gln Ser Asp Glu Gly Ser Ser Ser Gln  
 100 105 110  
 Lys Glu Glu Ser Pro Ser Thr Leu Gln Val Leu Pro Asp Ser Glu Ser  
 115 120 125  
 Leu Pro Arg Ser Glu Ile Asp Glu Lys Val Thr Asp Leu Val Gln Phe  
 130 135 140  
 Leu Leu Phe Lys Tyr Gln Met Lys Glu Pro Ile Thr Lys Ala Glu Ile  
 145 150 155 160  
 Leu Glu Ser Val Ile Lys Asn Tyr Glu Asp His Phe Pro Leu Leu Phe  
 165 170 175  
 Ser Glu Ala Ser Glu Cys Met Leu Leu Val Phe Gly Ile Asp Val Lys  
 180 185 190  
 Glu Val Asp Pro Thr Gly His Ser Phe Val Leu Val Thr Ser Leu Gly  
 195 200 205  
 Leu Thr Tyr Asp Gly Met Leu Ser Asp Val Gln Ser Met Pro Lys Thr  
 210 215 220  
 Gly Ile Leu Ile Leu Ile Leu Ser Ile Ile Phe Ile Glu Gly Tyr Cys  
 225 230 235 240  
 Thr Pro Glu Glu Val Ile Trp Glu Ala Leu Asn Met Met Gly Leu Tyr  
 245 250 255  
 Asp Gly Met Glu His Leu Ile Tyr Gly Glu Pro Arg Lys Leu Leu Thr  
 260 265 270  
 Gln Asp Trp Val Gln Glu Asn Tyr Leu Glu Tyr Arg Gln Val Pro Gly  
 275 280 285  
 Ser Asp Pro Ala Arg Tyr Glu Phe Leu Trp Gly Pro Arg Ala His Ala  
 290 295 300  
 Glu Ile Arg Lys Met Ser Leu Leu Lys Phe Leu Ala Lys Val Asn Gly  
 305 310 315 320  
 Ser Asp Pro Arg Ser Phe Pro Leu Trp Tyr Glu Glu Ala Leu Lys Asp  
 325 330 335  
 Glu Glu Glu Arg Ala Gln Asp Arg Ile Ala Thr Thr Asp Asp Thr Thr  
 340 345 350  
 Ala Met Ala Ser Ala Ser Ser Ser Ala Thr Gly Ser Phe Ser Tyr Pro  
 355 360 365  
 Glu

## (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 380 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1165170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Phe	Ser	Trp	Lys	Ala	Ser	Lys	Ala	Arg	Ser	Pro	Leu	Ser	Pro	Arg
1				5				10				15			
Tyr	Ser	Leu	Pro	Gly	Ser	Thr	Glu	Val	Leu	Thr	Gly	Cys	His	Ser	Tyr
						20			25			30			
Pro	Ser	Arg	Phe	Leu	Ser	Ala	Ser	Ser	Phe	Thr	Ser	Ala	Leu	Ser	Thr
						35			40			45			
Val	Asn	Met	Pro	Arg	Gly	Gln	Lys	Ser	Lys	Thr	Arg	Ser	Arg	Ala	Lys
						50			55			60			
Arg	Gln	Gln	Ser	Arg	Arg	Glu	Va1	Pro	Va1	Va1	Gln	Pro	Thr	Ala	Glu
						65			70			75			80
Glu	Ala	Gly	Ser	Ser	Pro	Va1	Asp	Gln	Ser	Ala	Gly	Ser	Ser	Phe	Pro
						85			90			95			
Gly	Gly	Ser	Ala	Pro	Gln	Gly	Va1	Lys	Thr	Pro	Gly	Ser	Phe	Gly	Ala
						100			105			110			
Gly	Val	Ser	Cys	Thr	Gly	Ser	Gly	Ile	Gly	Gly	Arg	Asn	Ala	Ala	Val
						115			120			125			
Leu	Pro	Asp	Thr	Lys	Ser	Ser	Asp	Gly	Thr	Gln	Ala	Gly	Thr	Ser	Ile
						130			135			140			
Gln	His	Thr	Leu	Lys	Asp	Pro	Ile	Met	Arg	Lys	Ala	Ser	Val	Leu	Ile
						145			150			155			160
Glu	Phe	Leu	Leu	Asp	Lys	Phe	Lys	Met	Lys	Glu	Ala	Val	Thr	Arg	Ser
						165			170			175			
Glu	Met	Leu	Ala	Val	Val	Asn	Lys	Lys	Tyr	Lys	Glu	Gln	Phe	Pro	Glu
						180			185			190			
Ile	Leu	Arg	Arg	Thr	Ser	Ala	Arg	Leu	Glu	Leu	Val	Phe	Gly	Leu	Glu
						195			200			205			
Leu	Lys	Glu	Ile	Asp	Pro	Ser	Thr	His	Ser	Tyr	Leu	Leu	Val	Gly	Lys
						210			215			220			
Leu	Gly	Leu	Ser	Thr	Glu	Gly	Ser	Leu	Ser	Ser	Asn	Trp	Gly	Leu	Pro
						225			230			235			240
Arg	Thr	Gly	Leu	Leu	Met	Ser	Val	Leu	Gly	Val	Ile	Phe	Met	Lys	Gly
						245			250			255			
Asn	Arg	Ala	Thr	Glu	Gln	Glu	Val	Trp	Gln	Phe	Leu	His	Gly	Val	Gly
						260			265			270			
Val	Tyr	Ala	Gly	Lys	Lys	His	Leu	Ile	Phe	Gly	Glu	Pro	Glu	Glu	Phe
						275			280			285			
Ile	Arg	Asp	Val	Val	Arg	Glu	Asn	Tyr	Leu	Glu	Tyr	Arg	Gln	Val	Pro
						290			295			300			
Gly	Ser	Asp	Pro	Pro	Ser	Tyr	Glu	Phe	Leu	Trp	Gly	Pro	Arg	Ala	His
						305			310			315			320
Ala	Glu	Thr	Thr	Lys	Met	Lys	Val	Leu	Glu	Val	Leu	Ala	Lys	Val	Asn
						325			330			335			
Gly	Thr	Val	Pro	Ser	Ala	Phe	Pro	Asn	Leu	Tyr	Gln	Leu	Ala	Leu	Arg
						340			345			350			
Asp	Gln	Ala	Gly	Gly	Val	Pro	Arg	Arg	Arg	Val	Gln	Gly	Lys	Gly	Val
						355			360			365			
His	Ser	Lys	Ala	Pro	Ser	Gln	Lys	Ser	Ser	Asn	Met				

370

375

380

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1040691

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Ser	Glu	Gln	Ser	Lys	Asp	Leu	Ser	Asp	Pro	Asn	Phe	Ala	Ala	Glu
1		5				10						15			
Ala	Pro	Asp	Cys	Glu	Met	Gln	Asp	Ser	Asp	Ala	Val	Pro	Val	Gly	Ile
					20			25					30		
Pro	Pro	Pro	Ala	Ser	Leu	Ala	Ala	Asn	Leu	Ala	Gly	Pro	Pro	Cys	Ala
						35		40				45			
Pro	Glu	Gly	Pro	Met	Ala	Ala	Gln	Gln	Ala	Ser	Pro	Pro	Pro	Glu	Glu
	50					55					60				
Arg	Ile	Glu	Asp	Val	Asp	Pro	Lys	Ile	Leu	Gln	Gln	Ala	Ala	Glu	Glu
65				70				75				80			
Gly	Arg	Ala	His	Gln	Pro	Gln	Ser	Pro	Ala	Arg	Pro	Ile	Pro	Ala	Pro
						85		90				95			
Pro	Ala	Pro	Ala	Gln	Leu	Val	Gln	Lys	Ala	His	Glu	Leu	Met	Trp	Tyr
					100			105				110			
Val	Leu	Val	Lys	Asp	Gln	Lys	Arg	Met	Val	Leu	Trp	Phe	Pro	Asp	Met
					115		120				125				
Val	Lys	Glu	Val	Met	Gly	Ser	Tyr	Lys	Trp	Cys	Arg	Ser	Ile	Leu	
	130					135				140					
Arg	Arg	Thr	Ser	Val	Ile	Leu	Ala	Arg	Val	Phe	Gly	Leu	His	Leu	Arg
145					150				155			160			
Leu	Thr	Asn	Leu	His	Thr	Met	Glu	Phe	Ala	Leu	Val	Lys	Ala	Leu	Ser
						165			170			175			
Pro	Glu	Glu	Leu	Asp	Arg	Val	Ala	Leu	Asn	Asn	Arg	Met	Pro	Met	Thr
						180		185				190			
Gly	Leu	Leu	Leu	Met	Ile	Leu	Ser	Leu	Ile	Tyr	Val	Lys	Gly	Arg	Gly
						195		200				205			
Ala	Arg	Glu	Gly	Ala	Val	Trp	Asn	Val	Leu	Arg	Ile	Leu	Gly	Leu	Arg
						210		215			220				
Pro	Trp	Lys	Lys	His	Ser	Thr	Phe	Gly	Asp	Val	Arg	Lys	Ile	Ile	Thr
225						230			235			240			
Glu	Glu	Phe	Val	Gln	Gln	Asn	Tyr	Leu	Lys	Tyr	Gln	Arg	Val	Pro	His
						245			250			255			
Ile	Glu	Pro	Pro	Glu	Tyr	Glu	Phe	Phe	Trp	Gly	Ser	Arg	Ala	Asn	Arg
						260		265			270				
Glu	Ile	Thr	Lys	Met	Gln	Ile	Met	Glu	Phe	Leu	Ala	Arg	Val	Phe	Lys
						275		280			285				
Lys	Asp	Pro	Gln	Ala	Trp	Pro	Ser	Arg	Tyr	Arg	Glu	Ala	Leu	Glu	Gln
						290		295			300				
Ala	Arg	Ala	Leu	Arg	Glu	Ala	Asn	Leu	Ala	Ala	Gln	Ala	Pro	Arg	Ser

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315